

-88	10	30	50
	GTTTGTCTCTGGGCAGCCAAGTTGGCATAATTGGAAGCTTTTCCGGGCTCTGGAGGAGGGT-29		
-28	70	90	110
-8	CCCTGCTTCTTCCTACAGCCGTTCCGGGCATGGCTGGCTGGGGGCGTCGCTCCACGTCT		31
	M A W L G A S L H V W		11
32	130	150	170
12	GGGGTTGGCTAATGCTCGGCAGCTGCCCTCCTGGCCAGAGCCCAGCTGGATTCTGATGGCA		91
	G W L M L G S C L L A R A Q L D S D G T		31
92	190	210	230
32	CCATCACTATAGAGGAGCAGATTGTCCTTGTGCTGAAAGCGAAAGTACAATGTGAACCTCA		151
	I T I E E Q I V L V L K A K V Q C E L N		51
152	250	270	
52	ACATCACAGCTCAACTCCAGGAGGGAGAAGTAATTGTTCCCTGAATGGGATGGACTCA		211
	I T A Q L Q E G E G N C F P E W D G L I		71
212	310	330	350
72	TTTGTGGCCAGAGGAACAGTGGGGAAATATCGGCTGTTCCAIGCCCTCCTTATATT		271
	C W P R G T V G K I S A V P C P Y I Y		91
272	370	390	410
92	ATGACTTCAACCATAAAGGAGTTGCTTCCGACACTGTAAACCCCAATGGAACATGGGATT		331
	D F N H K G V A F R H C N P N G T W D F		111

MATCH WITH FIG. 1B

FIG. 1A

MATCH WITH FIG. 1A

332	430	450	470	391
112	TTATGCACAGCTTAAATAAACATGGGCCAATTATTCAGACTGCCTTCGCTTTCGTCAGC			131
	M H S L N K T W A N Y S D C L R F L Q P			
392	490	510	530	451
132	CAGATATCAGCATAGGAAAGCAAGAAATCTGTGAACGCCCTCTATGTAATGTATACCGTTG			151
	D I S I G K Q E F C E R L Y V M Y T V G			
452	550	570	590	511
152	GCTACTCCATCICITTTGGTTCCTTGGCTGGCTATTCATCAATGGTTACTTCAGAC			171
	Y S I S F G S L A V A I L I I G Y F R R			
512	610	630	650	571
172	GATTGCATTGCACCTAGGAACCTATATCCACATGCACCTTATTTGTGCTTTCATGCTGAGAG			191
	L H C T R N Y I H M H L F V S F M L R A			
572	670	690	710	631
192	CTACAAGCATCTTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG			211
	T S I F V K D R V V H A H I G V K E L E			
632	730	750	770	691
212	AGTCCCTAATAATGCAGGATGACCCACAAAATTCATTGAGGCAACTTCTGTGGACAAAT			231
	S L I M Q D D P Q N S I E A T S V D K S			
790	810	830		

MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

692 CACAATATATCGGGTGCAAGATTGCTGTTGATGTTTATTACTTCTGGCTACAAATT 751
232 Q Y I G C K I A V V M F I Y F L A T N Y 251

850 870 890
752 ATTATTGGATCCTGGTGGAAGGTCTCTACCTGCATAATCTCATCTTTGTGGCTTCTTTT 811
252 Y W I L V E G L Y L H N L I F V A F F S 271

910 930 950
812 CGGACACCAATACTGTGGGGCTTTCATCTTGATAGGCTGGGGTTTCCAGCAGCATTTG 871
272 D T K Y L W G F I L I G W G F P A A F V 291

970 990 1010
872 TTGCAGCATGGGCTGTGGCAGCAACTCTGGCTGATGCGAGGTGCTGGGAACCTTAGTG 931
292 A A W A V A R A T L A D A R C W E L S A 311

1030 1050 1070
932 CTGGAGACATCAAGTGGATTATCAAGCACCGCATCTTAGCAGCTATTGGGCTGAATTTTA 991
312 G D I K W I Y Q A P I L A A I G L N F I 331

1090 1110 1130
992 TTCGTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAGTTG 1051
332 L F L N T V R V L A T K I W E T N A V G 351

1150 1170 1190
1052 GGCATGACACAAGGAAGCAATACAGGAACTGGCCAAATCGACACTGTCTGTCCTAG 1111
352 H D T R K Q Y R K L A K S T L V L V L V 371

MATCH WITH FIG. 1D

FIG. 1C

MATCH WITH FIG. 1C

1210	1230	1250	
1112 TCITGGAGTGCAATTACATCGTGTTCGTGCTGCCTCACTCCTTCACTGGGCTCGGT			1171
372 F G V H Y I V F V C L P H S F T G L G W			391
1270	1290	1310	
1172 GGGAGATCCGCATGCACTGTGAGCTCTTCTTCAACTCCTTTCAGGGTTTCTTTGTCTA			1231
392 E I R M H C E L F F N S F Q G F F V S I			411
1330	1350	1370	
1232 TCATCTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT			1291
412 I Y C Y C N G E V Q A E V K K M W S R W			431
1390	1410	1430	
1292 GGAATCTCTCCGTGGACTGGAAAAGACACCGCCATGTGGCAGCCGCAGATGCGGCTCAG			1351
432 N L S V D W K R T P P C G S R R C G S V			451
1450	1470	1490	
1352 TGCTACCAACCGTGACGCACAGCACCAAGATCGCCAGCAGCAGGTGGCGGCACACACGCAT			1411
452 L T T V T H S T S S Q S Q V A A A H A W			471
1510	1530	1550	
1412 GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAGCAGCAGCCTGACAGCCACATCAC			1471
472 C L S L A K L P R S P A D S L T A T S L			491

MATCH WITH FIG. 1E

FIG.1D

MATCH WITH FIG. 1D

1472	TTTACCTGGCIATGTCTGGAGTAACTCAGAGCAGGACTGCCTCACACACTCTCTCCACGA	1570	1590	1610	1531
492	Y L A M S G V T Q S R T A S H T L S T R				511
1532	GGAGCAACAAGGAAGATAGTGGGAGGCAGAGAGATGATATTCTAATGGAGAAGCCTTCCA	1630	1650	1670	1591
512	S N K E D S G R Q R D D I L M E K P S R				531
1592	GGCCTATGGAATCTAACCAGACACTGAAGGATGACAAGGAGAACTGAGGATGTTCTCT	1690	1710	1730	1651
532	P M E S N P D T E G				541
1652	GAATGGACATGTGTGGCTGACTTTCATGGGCTGGTCCCAATGGCTGTTGTGTGAGAGGGC	1750	1770	1790	1711
1712	TTGGCTGATACTCCCTATGCCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA	1810	1830	1850	1771
1772	TAATAGTTTTTtaggctccatgaattggctccctgtaaatactaacgacatgaaaaatgcaag	1870	1890	1910	1831
1832	TGTCAATGGAGTAGTTTATTACCTTCTATTGGCATCAAGTTTTCCTCTAAATTAATGTAT	1930	1950	1970	1891
1892	GGTATTGCTCTGTGATTGTTCA	1990			1914

FIG.1E

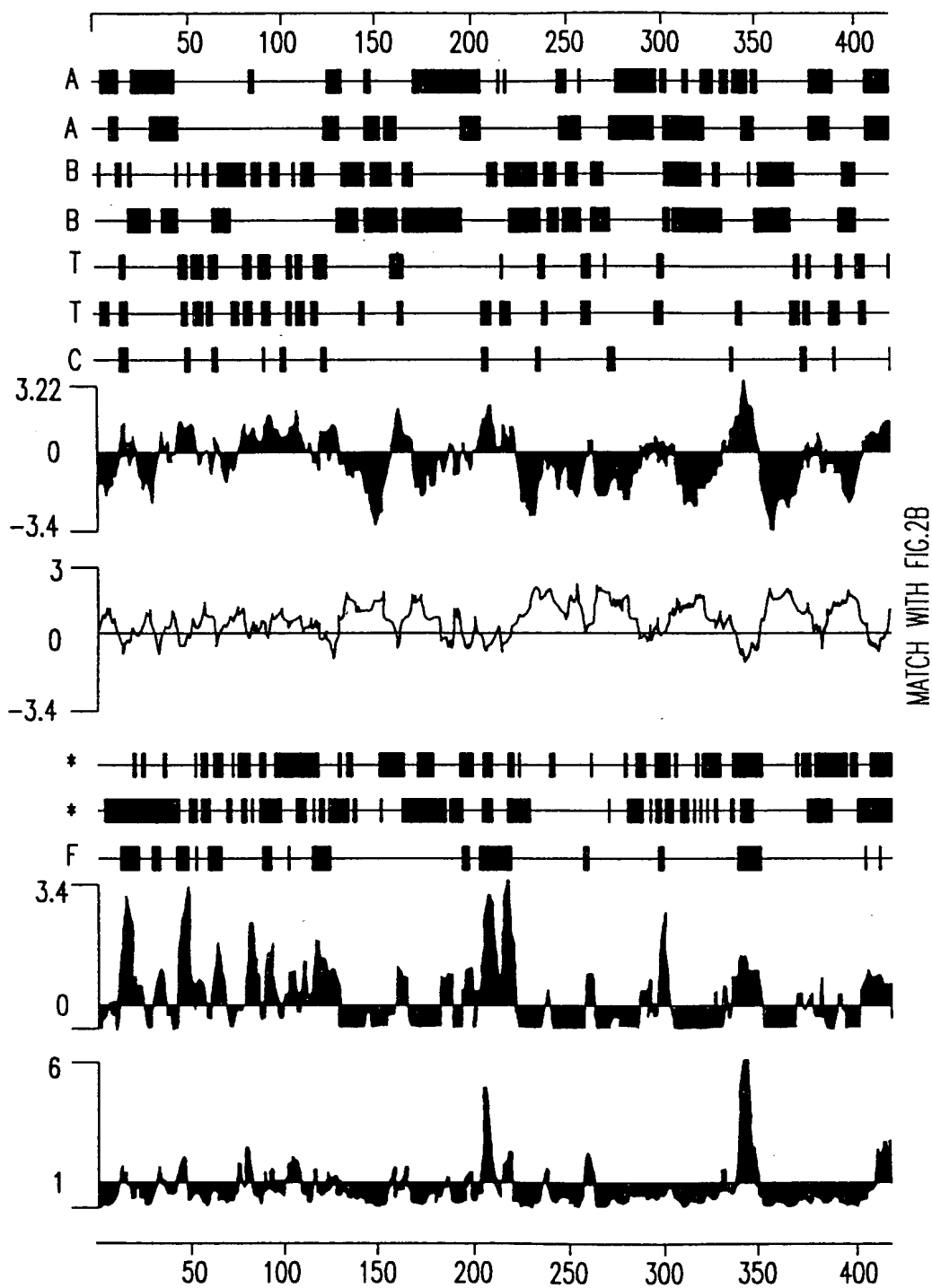


FIG. 2A

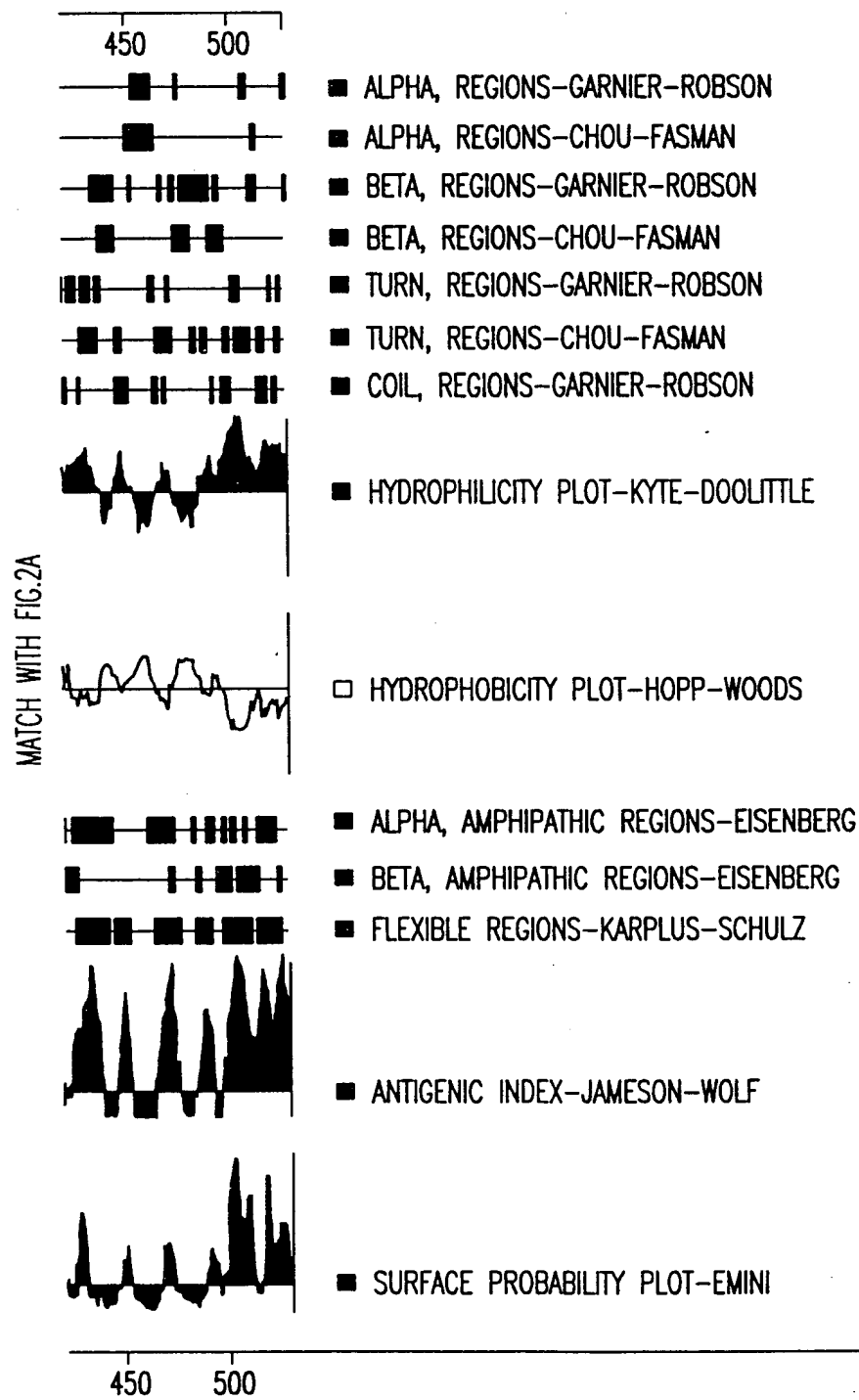


FIG. 2B

Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Probability P(N)	N
gp M74445 OPOPTH1_1	parathyroid hormone receptor [Di...]	597	8.2e-204	6
pir S A39286	parathyroid hormone / parathyroid...	597	2.9e-203	6
gp L04308 HUMPTH1_1	parathyroid hormone receptor [Ho...]	580	6.7e-190	5
pir S S29610	parathyroid hormone receptor - h...	580	6.1e-189	5
gp M77184 RATPATHYR1_1	parathyroid hormone receptor [Ra...]	576	7.7e-188	5
gp X78936 MPHPR1_1	parathyroid hormone/parathyroid ...	576	7.7e-188	5
pir S A42698	parathyroid hormone and parathyr...	576	7.7e-188	5
gp L34611 MUSPTH06_1	parathyroid hormone/parathyroid ...	576	4.1e-174	5
gp U11087 HSV1RG9_1	vasoactive intestinal peptide 1 ...	319	1.2e-98	5
gp M86835 RATVASREC1_1	vasoactive intestinal polypeptid...	254	3.1e-91	5

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTH1_1 parathyroid hormone receptor [Didelphis virginiana]
Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Match with FIG. 3B

FIG. 3A

Match with FIG. 3 A

Query: 729 IMQDDPQNSIEATSDKQYIGCKIAVVMFIYFLATNYYWILVEGLYLHNLIFVAFFSDT 908
 I +++ + E DK+ ++GC++AV +F+YFL TNYWILVEGLYLH+LIF+AFFS+

Sbjct: 253 ITEEELRAFTTEPPPADKAGFVGCRAVTVFLYFLTNYWILVEGLYLHSLIFMAFFSEK 312

Query: 909 KYLWGFILIGWGPAAFAVAWAVARATLADARCWELSGADIKWIYQAPILAAIGLNFILF 1088
 KYLWGF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFILF

Sbjct: 313 KYLWGFTLFGWGLPAVFVAVVTVRATLANTECWDLSSGNKKWIIQVPILAAIVVNFILF 372

Query: 1089 LNTVRVLATKIWETNAVGHDTQRKQYRKLAKSTLVLVFGVHYIVFVCLPHS 1244

+N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++

Sbjct: 373 INIIRVLATKLRETNAGRCSTRQYRKLKSTLVLMPLFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGAFRHCNPNGTWDFMHSLNKTW 446
 +G C PEWD ++CWP G GK+ AVPCP YIYDFNHHKG A+R C+ NG+W+ + N+TW

Sbjct: 102 DGFCLPEWDNIVCWPAGVPGKVAVPCPDYIYDFNHHKGRAYRRCDSNGSWELVPGNNRTW 161

Query: 447 ANYSDCLRFL 476

ANYS+C++FL

Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KQEFCERLVVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYYIHMHLFVSFMLRATSIFV 677
 ++E +RL ++YTVGYSIS GSL VA+LI+GYFRRLHCTRNYYIHMHLFVSFMLRA SIF+

Match with FIG. 3 C

FIG. 3B

MATCH WITH FIG. 3B

Sbjct: 177 EREVFDRGLMIYTVGYSISGLSLTVAVLILGYFRRLHCTRNVIHHLFVSFMLRAVSIFI 236

Query: 678 KDRVVHAHIGVKELESIMQD 740

KD V+++ + E+E + ++

Sbjct: 237 KDAVLYSGVSTDEIERITEEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFNFNSFQGFFVSIICYCNGEVQAEVKKMSRWNLSDWKRTPPCGS 1424

+G+ W++++MH E+ FNSFQGFV+IIYC+CNGEVQAE+KK WSRW L++D+KR GS

Sbjct: 427 SGILWQVMHYEMLFNSFQGFVSIICYCNGEVQAEIKKSWRWTALDFKRRKARSGS 485

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query: 159 AQLSDSGTTITIEEQIVLVKAKVQCELNITAQLQEGE 269

A +D+D IT EEQI+L+ A+ QCE + L+ E

Sbjct: 24 ALVDADDVITKEEQIILLRNAQAQCEQRLKEVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPDSHITLPGYV 1576

+S + A A + H LPGYV

Sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

FIG. 3C